SEQUENCE LISTING

<110> WUCHERPFENNIG, Kai W
STROMINGER, Jack L

<120> MONOVALENT, MULTIVALENT AND MULTIMERIC MHC BINDING DOMAIN FUSION PROTEINS AND CONJUGATES, AND USES THEREFOR

<130> HUIP-P01-005

<140> 09/248,964
<141> 1999-02-12

<150> PCT/US97/14503
<151> 1997-08-15

<150> 60/075,351
<151> 1998-02-19

<150> 60/024,077
<151> 1996-08-15

<160> 14

<170> PatentIn Ver. 2.0

<210> 1
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-Fos fusion

<220>
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<222> (1)..(735)

<220>
<221> misc_feature
<222> (1)..(21)
<223> 3' end of secretory signal

<220>
<221> misc_structure
<222> (22)..(594)
<223> DRA*0101 extracellular domain

<220>
<221> misc_feature
<222> (595)..(615)
<223> Linker sequence

<220>
<221> misc_feature
<222> (616)..(735)
<223> Fos leucine zipper domain

<400> 1

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gta tct ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag   48
Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln
  1               5                  10                  15

gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac   96
Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
             20                  25                  30

ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg   144
Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
         35                  40                  45

gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa   192
Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
     50                  55                  60

ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg   240
Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
 65                  70                  75                  80

aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta   288
Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
                 85                  90                  95

act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc   336
Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
            100                 105                 110

atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg   384
Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
        115                 120                 125

ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc   432
Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
    130                 135                 140

ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc   480
Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
145                 150                 155                 160

ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc   528
Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
                165                 170                 175

ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct   576
Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
            180                 185                 190

ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat   624
Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp
        195                 200                 205

aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg   672
Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu
    210                 215                 220
```

```
cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc   720
Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
225                 230                 235                 240

atc ctg gcc gcc cat tgagaattct atgac                            750
Ile Leu Ala Ala His
                245
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<210> 2
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-Fos fusion

<220>
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<223> 3' end of secretory signal

<220>
<221> misc_structure
<222> (8)..(198)
<223> DRA*0101 extracellular domain

<220>
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<222> (199)..(205)
<223> Linker sequence

<220>
<221> misc_feature
<222> (206)..(245)
<223> Fos leucine zipper domain

<400> 2

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Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln
  1               5                  10                  15

Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
             20                  25                  30

Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
         35                  40                  45

Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
     50                  55                  60

Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
 65                  70                  75                  80

Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
                 85                  90                  95

Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
            100                 105                 110
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```
Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
        115                 120                 125

Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
    130                 135                 140

Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
145                 150                 155                 160

Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
                165                 170                 175

Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
            180                 185                 190

Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp
        195                 200                 205

Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu
    210                 215                 220

Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
225                 230                 235                 240

Ile Leu Ala Ala His
                245
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<210> 3
<211> 771
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-Jun fusion

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<222> (1)..(756)

<220>
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<222> (1)..(21)
<223> 3' end of secretory signal

<220>
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<222> (22)..(615)
<223> DRB1*1501 extracellular domain

<220>
<221> misc_feature
<222> (616)..(636)
<223> Linker sequence

<220>
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<222> (637)..(756)

<223> Jun leucine zipper domain

<400> 3

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gta tct ctc gag aaa aga gag ggg gac acc cga cca cgt ttc ctg tgg   48
Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp
  1               5                  10                  15

cag cct aag agg gag tgt cat ttc ttc aat ggg acg gag cgg gtg cgg   96
Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
             20                  25                  30

ttc ctg gac aga tac ttc tat aac cag gag gag tcc gtg cgc ttc gac  144
Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
         35                  40                  45

agc gac gtg ggg gag ttc cgg gcg gtg acg gag ctg ggg cgg cct gac  192
Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
     50                  55                  60

gct gag tac tgg aac agc cag aag gac atc ctg gag cag gcg cgg gcc  240
Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
 65                  70                  75                  80

gcg gtg gac acc tac tgc aga cac aac tac ggg gtt gtg gag agc ttc  288
Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
                 85                  90                  95

aca gtg cag cgg cga gtc caa cct aag gtg act gta tat cct tca aag  336
Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
            100                 105                 110

acc cag ccc ctg cag cac cac aac ctc ctg gtc tgc tct gtg agt ggt  384
Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
        115                 120                 125

ttc tat cca ggc agc att gaa gtc agg tgg ttc ctg aac ggc cag gaa  432
Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
    130                 135                 140

gag aag gct ggg atg gtg tcc aca ggc ctg atc cag aat gga gac tgg  480
Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
145                 150                 155                 160

acc ttc cag acc ctg gtg atg ctg gaa aca gtt cct cga agt gga gag  528
Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
                165                 170                 175

gtt tac acc tgc caa gtg gag cac cca agc gtg aca agc cct ctc aca  576
Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
            180                 185                 190

gtg gaa tgg aga gca cgg tct gaa tct gca cag agc aag gtc gac gga  624
Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
        195                 200                 205
```

```
ggt ggc ggc ggt cgc atc gcc cgg ctc gag gaa aaa gtg aaa acc ttg   672
Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
    210                 215                 220

aaa gct cag aac tcg gag ctc gcg tcc acg gcc aac atg ctc agg gaa   720
Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
225                 230                 235                 240

cag gtg gca cag ctt aaa cag aaa gtc atg aac cat tgagaattct atgac  771
Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
                245                 250
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-Jun fusion

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<223> 3' end of secretory signal

<220>
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<222> (8)..(205)
<223> DRB1*1501 extracellular domain

<220>
<221> misc_feature
<222> (206)..(212)
<223> Linker sequence

<220>
<221> misc_feature
<222> (213)..(252)
<223> Jun leucine zipper domain

<400> 4

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Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp
  1               5                  10                  15

Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
             20                  25                  30

Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
         35                  40                  45

Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
     50                  55                  60

Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
 65                  70                  75                  80
```

Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
85 90 95

Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
100 105 110

Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
115 120 125

Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
130 135 140

Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
145 150 155 160

Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
165 170 175

Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
180 185 190

Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
195 200 205

Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
210 215 220

Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
225 230 235 240

Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
245 250

<210> 5
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 5
gtatctctcg agaaaagaga gatcaaagaa gaacatgtga tc 42

<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 6
gtcatagaat tctcaatggg cggccaggat gaactccag 39

<210> 7
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 7
gtatctctcg agaaaagaga gggggacacc cgaccacgtt tc 42

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 8
gtcatagaat tctcaatggt tcatgacttt ctgtttaag 39

<210> 9
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic, biotin ligase recognition sequence

<400> 9
Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp
1 5 10

<210> 10
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic, linker sequence

<400> 10
Ser Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 11
<211> 1446

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-IgG fusion

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<222> (16)..(588)
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<222> (589)..(609)
<223> Linker

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<222> (610)..(729)
<223> Fos leucine zipper domain

<220>
<221> misc_feature
<222> (730)..(1437)
<223> IgG domain

<400> 11

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ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag gcc gag   48
Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu
  1               5                  10                  15

ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac ttt gat   96
Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
             20                  25                  30

ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg gtc tgg   144
Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
         35                  40                  45

cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa ggt gca   192
Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
     50                  55                  60

ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg aca aag   240
Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
 65                  70                  75                  80
```

```
cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta act gtg   288
Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
                 85                  90                  95

ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc atc tgt   336
Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
            100                 105                 110

ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg ctt cga   384
Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg
        115                 120                 125

aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc ctg ccc   432
Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro
    130                 135                 140

agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc ctg ccc   480
Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro
145                 150                 155                 160

tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc ttg gat   528
Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp
                165                 170                 175

gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct ctc cca   576
Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro
            180                 185                 190

gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat aca ctc   624
Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp Thr Leu
        195                 200                 205

caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg cag acc   672
Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr
    210                 215                 220

gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc atc ctg   720
Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu
225                 230                 235                 240

gcc gcc cat gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt   768
Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
                245                 250                 255

cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc   816
Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
            260                 265                 270

ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc   864
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
        275                 280                 285

ccc ata gtc aca tgt gtg gtg gtg gat gtg agc gag gat gac cca gat   912
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
    290                 295                 300
```

```
gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag   960
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
305                 310                 315                 320

aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt   1008
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
                325                 330                 335

gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa   1056
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
            340                 345                 350

tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc   1104
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
        355                 360                 365

tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct   1152
Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
    370                 375                 380

cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg   1200
Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
385                 390                 395                 400

gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac   1248
Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
                405                 410                 415

ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct   1296
Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
            420                 425                 430

gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac   1344
Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
        435                 440                 445

tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg   1392
Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
    450                 455                 460

cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt aaa       1437
His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
465                 470                 475

tgagaattc                                                        1446
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<210> 12
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-IgG fusion

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<222> (1)..(5)
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<222> (6)..(196)
<223> DRA*0101 extracellular domain

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<222> (197)..(203)
<223> Linker

<220>
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<222> (204)..(243)
<223> Fos leucine zipper domain

<220>
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<222> (244)..(479)
<223> IgG domain

<400> 12

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Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu
  1               5                  10                  15

Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
             20                  25                  30

Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
         35                  40                  45

Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
     50                  55                  60

Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
 65                  70                  75                  80

Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
                 85                  90                  95

Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
            100                 105                 110

Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg
        115                 120                 125

Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro
    130                 135                 140

Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro
145                 150                 155                 160

Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp
```

```
                165                 170                 175

Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro
            180                 185                 190

Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu Thr Asp Thr Leu
        195                 200                 205

Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr
    210                 215                 220

Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu
225                 230                 235                 240

Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
                245                 250                 255

Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
            260                 265                 270

Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
        275                 280                 285

Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
    290                 295                 300

Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
305                 310                 315                 320

Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
                325                 330                 335

Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
            340                 345                 350

Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
        355                 360                 365

Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
    370                 375                 380

Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
385                 390                 395                 400

Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
                405                 410                 415

Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
            420                 425                 430

Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
        435                 440                 445

Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
    450                 455                 460

His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
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465 470 475

<210> 13
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-IgM fusion

<220>
<221> CDS
<222> (1)..(1836)

<220>
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<222> (1)..(75)
<223> 3' end of secretory signal

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<223> DRA*0101 extracellular domain

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<222> (670)..(789)
<223> Fos leucine zipper domain

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<222> (790)..(1836)
<223> IgG domain

<400> 13

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atg gcc ata agt gga gtc cct gtg cta gga ttt ttc atc ata gct gtg   48
Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
  1               5                  10                  15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc   96
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
             20                  25                  30

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg   144
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
         35                  40                  45

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag   192
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
     50                  55                  60
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gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag   240
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65                  70                  75                  80

gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa   288
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
                85                  90                  95

atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca   336
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
            100                 105                 110

gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac   384
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
        115                 120                 125

gtc ctc atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc   432
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
    130                 135                 140

acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca   480
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145                 150                 155                 160

gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc   528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
                165                 170                 175

ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac   576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
            180                 185                 190

tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca   624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
        195                 200                 205

agc cct ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta   672
Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu
    210                 215                 220

act gat aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct   720
Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
225                 230                 235                 240

gcg ttg cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg   768
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
                245                 250                 255

gag ttc atc ctg gcc gcc cac gtc gca gaa atg aac ccc aat gta aat   816
Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn
            260                 265                 270

gtg ttc gtc cca cca cgg gat ggc ttc tct ggc cct gca cca cgc aag   864
Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys
        275                 280                 285

tct aaa ctc atc tgc gag gcc acg aac ttc act cca aaa ccg atc aca   912
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Ser Lys Leu Ile Cys Glu Ala Thr Asn Phe Thr Pro Lys Pro Ile Thr
    290                 295                 300

gta tcc tgg cta aag gat ggg aag ctc gtg gaa tct ggc ttc acc aca   960
Val Ser Trp Leu Lys Asp Gly Lys Leu Val Glu Ser Gly Phe Thr Thr
305                 310                 315                 320

gat ccg gtg acc atc gag aac aaa gga tcc aca ccc caa acc tac aag   1008
Asp Pro Val Thr Ile Glu Asn Lys Gly Ser Thr Pro Gln Thr Tyr Lys
                325                 330                 335

gtc ata agc aca ctt acc atc tct gaa atc gac tgg ctg aac ctg aat   1056
Val Ile Ser Thr Leu Thr Ile Ser Glu Ile Asp Trp Leu Asn Leu Asn
            340                 345                 350

gtg tac acc tgc cgt gtg gat cac agg ggt ctc acc ttc ttg aag aac   1104
Val Tyr Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Leu Lys Asn
        355                 360                 365

gtg tcc tcc aca tgt gct gcc agt ccc tcc aca gat atc ctt aat ttt   1152
Val Ser Ser Thr Cys Ala Ala Ser Pro Ser Thr Asp Ile Leu Asn Phe
    370                 375                 380

act att cct cct tcc ttt gcc gac atc ttc ctt agc aag tcc gct aac   1200
Thr Ile Pro Pro Ser Phe Ala Asp Ile Phe Leu Ser Lys Ser Ala Asn
385                 390                 395                 400

ctg acc tgt ctg gtc tca aac ctg gca acc tat gaa acc ctg agt atc   1248
Leu Thr Cys Leu Val Ser Asn Leu Ala Thr Tyr Glu Thr Leu Ser Ile
                405                 410                 415

tcc tgg gct tct caa agt ggt gaa cca ctg gaa acc aaa att aaa atc   1296
Ser Trp Ala Ser Gln Ser Gly Glu Pro Leu Glu Thr Lys Ile Lys Ile
            420                 425                 430

atg gaa agc cat ccc aat ggc acc ttc agt gct aag ggt gtg gct agt   1344
Met Glu Ser His Pro Asn Gly Thr Phe Ser Ala Lys Gly Val Ala Ser
        435                 440                 445

gtt tgt gtg gaa gac tgg aat aac agg aag gaa ttt gtg tgt act gtg   1392
Val Cys Val Glu Asp Trp Asn Asn Arg Lys Glu Phe Val Cys Thr Val
    450                 455                 460

act cac agg gat ctg cct tca cca cag aag aaa ttc atc tca aaa ccc   1440
Thr His Arg Asp Leu Pro Ser Pro Gln Lys Lys Phe Ile Ser Lys Pro
465                 470                 475                 480

aat gag gtg cac aaa cat cca cct gct gtg tac ctg ctg cca cca gct   1488
Asn Glu Val His Lys His Pro Pro Ala Val Tyr Leu Leu Pro Pro Ala
                485                 490                 495

cgt gaa caa ctg aac ctg agg gag tca gcc aca gtc acc tgc ctg gtg   1536
Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Val Thr Cys Leu Val
            500                 505                 510

aag ggc ttc tct cct gca gac atc tct gtg caa tgg aag cag agg ggc   1584
Lys Gly Phe Ser Pro Ala Asp Ile Ser Val Gln Trp Lys Gln Arg Gly
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        515                 520                 525
cag ctc tta ccc cag gag aag tat gtg acc agt gcc ccg atg cca gag   1632
Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu
    530                 535                 540

cct ggg gcc cca ggc ttc tac ttt acc cac agc atc ctg act gtg aca   1680
Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr
545                 550                 555                 560

gag gag gaa tgg aac tcc gga gag acc tat acc tgt gtt gta ggc cac   1728
Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His
                565                 570                 575

gag gcc ctg cca cac ctg gtg acc gag agg acc gtg gac aag tcc act   1776
Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr
            580                 585                 590

ggt aaa ccc aca ctg tac aat gtc tcc ctg atc atg tct gac aca ggc   1824
Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
        595                 600                 605

ggc acc tgc tat tgaagatctg tcgac                                  1851
Gly Thr Cys Tyr
    610
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<223> IgG domain

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Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
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Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
             20                  25                  30

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
         35                  40                  45

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
     50                  55                  60

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65                  70                  75                  80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
                 85                  90                  95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
            100                 105                 110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
        115                 120                 125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
    130                 135                 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145                 150                 155                 160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
                165                 170                 175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
            180                 185                 190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
        195                 200                 205

Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu
    210                 215                 220

Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
225                 230                 235                 240

Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
                245                 250                 255

Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn
            260                 265                 270


Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys
        275                 280                 285
```

```
Ser Lys Leu Ile Cys Glu Ala Thr Asn Phe Thr Pro Lys Pro Ile Thr
    290                 295                 300

Val Ser Trp Leu Lys Asp Gly Lys Leu Val Glu Ser Gly Phe Thr Thr
305                 310                 315                 320

Asp Pro Val Thr Ile Glu Asn Lys Gly Ser Thr Pro Gln Thr Tyr Lys
                325                 330                 335

Val Ile Ser Thr Leu Thr Ile Ser Glu Ile Asp Trp Leu Asn Leu Asn
            340                 345                 350

Val Tyr Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Leu Lys Asn
        355                 360                 365

Val Ser Ser Thr Cys Ala Ala Ser Pro Ser Thr Asp Ile Leu Asn Phe
    370                 375                 380

Thr Ile Pro Pro Ser Phe Ala Asp Ile Phe Leu Ser Lys Ser Ala Asn
385                 390                 395                 400

Leu Thr Cys Leu Val Ser Asn Leu Ala Thr Tyr Glu Thr Leu Ser Ile
                405                 410                 415

Ser Trp Ala Ser Gln Ser Gly Glu Pro Leu Glu Thr Lys Ile Lys Ile
            420                 425                 430

Met Glu Ser His Pro Asn Gly Thr Phe Ser Ala Lys Gly Val Ala Ser
        435                 440                 445

Val Cys Val Glu Asp Trp Asn Asn Arg Lys Glu Phe Val Cys Thr Val
    450                 455                 460

Thr His Arg Asp Leu Pro Ser Pro Gln Lys Lys Phe Ile Ser Lys Pro
465                 470                 475                 480

Asn Glu Val His Lys His Pro Pro Ala Val Tyr Leu Leu Pro Pro Ala
                485                 490                 495

Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Val Thr Cys Leu Val
            500                 505                 510

Lys Gly Phe Ser Pro Ala Asp Ile Ser Val Gln Trp Lys Gln Arg Gly
        515                 520                 525

Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu
    530                 535                 540

Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr
545                 550                 555                 560

Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His
                565                 570                 575

Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr
            580                 585                 590
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Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
595 600 605

Gly Thr Cys Tyr
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